

The embodiments of the invention in which an exclusive property or privilege is claimed are defined as follows:

1. A plant breeding method comprising:
 - (a) mixing pollen obtained from a breeding group comprising a plurality of parental plants to obtain a pollen polymix;
 - (b) pollinating female reproductive structures from each parental plant in the plurality of parental plants with the pollen polymix to obtain a plurality of progeny lots, wherein each progeny lot comprises seeds obtained from a different cross between the pollen polymix and each different parental plant of the plurality of parental plants;
 - (c) evaluating progeny plants grown from each of the progeny lots using objective criteria to obtain a phenotype score;
 - (d) determining the pedigree of a plurality of progeny plants using molecular parental analysis; and
 - (e) using the pedigree and phenotype score to identify elite plants for use in a next generation of plant breeding.
2. The method of Claim 1 additionally comprising selecting candidate plants from within the progeny plants based upon their phenotype score, wherein step (d) is performed on the candidate plants, and step (e) is performed using the pedigree and phenotype scores from the candidate plants to identify elite plants for use in a next generation of plant breeding.
3. The method of Claim 1 wherein the pedigree and phenotype scores are used to estimate the breeding values of a plurality of progeny and parental plants, and the breeding values are used to identify the elite plants for use in a next generation of plant breeding.
4. The method of Claim 3, wherein the elite plants are derived from parental plants that have a high general combining ability.
5. The method of Claim 1 wherein the pedigree determined is paternity.
6. The method of Claim 1 wherein the pedigree determined is paternity and maternity.

7. The method of Claim 1 wherein the phenotype score is obtained for a phenotype selected from the group consisting of disease resistance, growth rate, growth habit, chemical composition of any plant tissue, drought resistance, temperature hardiness, elevation adaptation, fecundity, and any combination thereof.

8. The method of Claim 1 wherein the molecular parental analysis is selected from the group consisting of genomic DNA analysis, RNA analysis, cDNA analysis, protein analysis, secondary compound analysis and any combination thereof.

9. The method of Claim 8 wherein the DNA analysis is performed using a DNA analysis method selected from the group of DNA sequencing, restriction fragment length polymorphism (RFLP), amplified fragment length polymorphism (AFLP), randomly amplified polymorphic DNA (RAPD), single nucleotide repeat microsatellites (i.e., simple sequence repeats (SSR)), di-, tri-, and tetra- nucleotide repeat SSRs, SSR-anchored PCR, sequenced tagged sites (STS), single nucleotide polymorphism (SNP), single stranded conformational polymorphism (SSCP), sequenced characterized amplified regions (SCAR), allele-specific associated primers (ASAP), single primer amplification reaction (SPARs), and cleaved amplified polymorphic sequences (CAP).

10. The method of Claim 1, wherein a plurality of pollen polymixes are prepared, each pollen polymix comprised of pollen obtained from a plurality of different parental plants, each pollen polymix of the plurality of pollen polymixes being used to pollinate female reproductive structures from parental plants whose pollen or that of its close relatives are not represented in the pollinating pollen polymix.

11. A method of evaluating plant progeny resulting from a pollen polymix cross comprising:

- (a) evaluating progeny plants grown from a plurality of progeny seed lots obtained from a pollen polymix crossed to a plurality of parental plants using objective criteria to obtain a phenotype score;
- (b) determining the pedigree of the progeny plants using molecular parental analysis;

(c) estimating the breeding value of the progeny plants using pedigree and at least one plant phenotype; and

(d) using the breeding value to identify elite plants for use in a next generation of plant breeding.

12. The method of Claim 11 additionally comprising selecting candidate plants from within the progeny plants based upon their estimated breeding value, wherein step (b) is performed on the candidate plants.

13. The method of Claim 11 wherein the pedigree determined is paternity.

14. The method of Claim 11 wherein the pedigree determined is paternity and maternity.

15. The method of Claim 11 wherein the phenotype used to estimate progeny plant breeding value is selected from the group consisting of disease resistance, growth rate, growth habit, chemical composition of any plant tissue, drought resistance, temperature hardiness, elevation adaptation, fecundity, and any combination thereof.

16. The method of Claim 11 wherein the molecular parental analysis is selected from the group consisting of genomic DNA analysis, RNA analysis, cDNA analysis, protein analysis, secondary compound analysis and any combination thereof.

17. The method of Claim 15 wherein the DNA analysis is performed using a DNA analysis method selected from the group of DNA sequencing, restriction fragment length polymorphism (RFLP), amplified fragment length polymorphism (AFLP), randomly amplified polymorphic DNA (RAPD), single nucleotide repeat microsatellites (i.e., simple sequence repeats (SSR)), di-, tri-, and tetra- nucleotide repeat SSRs, SSR-anchored PCR, sequenced tagged sites (STS), single nucleotide polymorphism (SNP), single stranded conformational polymorphism (SSCP), sequenced characterized amplified regions (SCAR), allele-specific associated primers (ASAP), single primer amplification reaction (SPARs), and cleaved amplified polymorphic sequences (CAP).

18. The method of Claim 11, wherein the elite plants are derived from parental plants that have a high general combining ability.

19. The method of Claim 11, wherein the progeny plants are obtained from a pollen polymix cross performed with a plurality of pollen polymixes, each pollen polymix comprised of pollen obtained from a plurality of different parental plants, the plurality of pollen polymixes each being used to pollinate female reproductive structures from parental plants whose pollen or that of its close relatives are not represented in the pollinating pollen polymix.

20. A tree breeding method comprising:

(a) mixing pollen obtained from a breeding group comprising a plurality of parental trees to obtain a pollen polymix;

(b) pollinating female reproductive structures from each parental tree in the plurality of parental trees with the pollen polymix to obtain a plurality of progeny lots, wherein each progeny lot comprises seeds obtained from a different cross between the pollen polymix and each different parental tree of the plurality of parental trees;

(c) evaluating progeny trees grown from each of the progeny lots using objective criteria to obtain a phenotype score;

(d) determining the pedigree of a plurality of progeny trees using DNA analysis; and

(e) using the pedigree and phenotype score to identify elite trees for use in a next generation of tree breeding.

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